

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING ERROR REPORT**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:**

Application Serial Number: 10/582,973  
Source: IFWP  
Date Processed by STIC: 6/26/06

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

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**ERROR DETECTED**
**SUGGESTED CORRECTION**
**SERIAL NUMBER:**

*10/582,973*

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1  Wrapped Nucleic  
Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2  Invalid Line Length      The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3  Misaligned Amino  
Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. **Do not use tab codes between numbers;** use **space characters**, instead.
- 4  Non-ASCII      The submitted file was **not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.**
- 5  Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6  PatentIn 2.0  
"bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7  Skipped Sequences  
(OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for **each** skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8  Skipped Sequences  
(NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for **each** skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9  Use of n's or Xaa's  
(NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10  Invalid <213>  
Response      Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11  Use of <220>  
*4-8*      Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12  PatentIn 2.0  
"bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13  Misuse of n/Xaa      "n" **can only represent a single nucleotide;** "Xaa" **can only represent a single amino acid**



IFWP

**RAW SEQUENCE LISTING**  
PATENT APPLICATION: US/10/582,973

DATE: 06/26/2006  
TIME: 13:30:45

Input Set : A:\sequence list.txt  
Output Set: N:\CRF4\06262006\J582973.raw

2 <110> APPLICANT: Toshikazu Nakamura  
 W--> 3 <120> TITLE OF INVENTION: Glycosylation-deficient hepatocyte growth factor  
 W--> 4 <130> FILE REFERENCE: N13F1456  
 C--> 5 <140> CURRENT APPLICATION NUMBER: US/10/582,973  
 C--> 5 <141> CURRENT FILING DATE: 2006-06-15  
 W--> 5 <160> NUMBER OF SEQ ID: 8

**ERRORED SEQUENCES**

106 <210> SEQ ID NO: 2  
 107 <211> LENGTH: 723  
 108 <212> TYPE: PRT  
 109 <213> ORGANISM: Homo sapiens  
 W--> 110 <220> FEATURE: Hepatocyte growth factor of five amino acids-deleted type  
 111 <223> OTHER INFORMATION:  
 W--> 112 <400> SEQUENCE: 2  
 113 Met Trp Val Thr Lys Leu Leu Pro Ala Leu Leu Gln His Val Leu  
 114 5 10 15  
 115 Leu His Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln  
 116 20 25 30  
 117 Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys Thr  
 118 35 40 45  
 119 Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys Val  
 120 50 55 60  
 121 Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly Leu  
 122 65 70 75 80  
 123 Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln Cys  
 124 85 90 95  
 125 Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu Phe  
 126 100 105 110  
 127 Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys  
 128 115 120 125  
 129 Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr Lys  
 130 130 135 140  
 131 Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu His  
 132 145 150 155 160  
 133 Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr Cys Arg Asn Pro Arg  
 134 165 170 175  
 135 Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser Asn Pro Glu Val Arg  
 136 180 185 190  
 137 Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu Cys Met Thr  
 138 195 200 205

*see p. 3, too*  
*move this to 12237 line. 12207*  
*Does Not Comply*  
*Corrected Diskette Needed*  
*never has*  
*a response.*  
*It is a*  
*"header" only.*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/582,973

DATE: 06/26/2006  
TIME: 13:30:45

Input Set : A:\sequence list.txt  
Output Set: N:\CRF4\06262006\J582973.raw

139 Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp His Thr Glu Ser Gly  
140 210 215 220  
141 Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro His Arg His Lys Phe  
142 225 230 235 240  
143 Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp Asp Asn Tyr Cys Arg  
144 245 250 255  
145 Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr Thr Leu Asp Pro His  
146 260 265 270  
147 Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys Ala Asp Asn Thr Met  
148 275 280 285  
149 Asn Asp Thr Asp Val Pro Leu Glu Thr Thr Glu Cys Ile Gln Gly Gln  
150 290 295 300  
151 Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr Ile Trp Asn Gly Ile Pro  
152 305 310 315 320  
153 Cys Gln Arg Trp Asp Ser Gln Tyr Pro His Glu His Asp Met Thr Pro  
154 325 330 335  
155 Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu Asn Tyr Cys Arg Asn Pro  
156 340 345 350  
157 Asp Gly Ser Cys Ser Pro Trp Cys Phe Thr Thr Asp Pro Asn Ile Arg  
158 355 360 365  
159 Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys Asp Met Ser His Gly Gln  
160 370 375 380  
161 Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr Met Gly Asn Leu Ser Gln  
162 385 390 395 400  
163 Thr Arg Ser Gly Leu Thr Cys Ser Met Trp Asp Lys Asn Met Glu Asp5  
164 405 410 415  
165 Leu His Arg His Ile Phe Trp Glu Pro Asp Ala Ser Lys Leu Asn Glu  
166 420 425 430  
167 Asn Tyr Cys Arg Asn Pro Asp Asp Ala His Gly Pro Trp Cys Tyr  
168 435 440 445  
169 Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys Pro Ile Ser Arg Cys  
170 450 455 460  
171 Glu Gly Asp Thr Thr Pro Thr Ile Val Asn Leu Asp His Pro Val Ile  
172 465 470 475 480  
173 Ser Cys Ala Lys Thr Lys Gln Leu Arg Val Val Asn Gly Ile Pro Thr  
174 485 490 495  
175 Arg Thr Asn Ile Gly Trp Met Val Ser Leu Arg Tyr Arg Asn Lys His  
176 500 505 510  
177 Ile Cys Gly Gly Ser Leu Ile Lys Glu Ser Trp Val Leu Thr Ala Arg  
178 515 520 525  
179 Gln Cys Phe Pro Ser Arg Asp Leu Lys Asp Tyr Glu Ala Trp Leu Gly  
180 530 535 540  
181 Ile His Asp Val His Gly Arg Gly Asp Glu Lys Cys Lys Gln Val Leu  
182 545 550 555 560  
183 Asn Val Ser Gln Leu Val Tyr Gly Pro Glu Gly Ser Asp Leu Val Leu  
184 565 570 575  
185 Met Lys Leu Ala Arg Pro Ala Val Leu Asp Asp Phe Val Ser Thr Ile  
186 580 585 590  
187 Asp Leu Pro Asn Tyr Gly Cys Thr Ile Pro Glu Lys Thr Ser Cys Ser

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/582,973

DATE: 06/26/2006  
TIME: 13:30:45

Input Set : A:\sequence list.txt  
Output Set: N:\CRF4\06262006\J582973.raw

188	595	600	605
189	Val Tyr Gly Trp Gly Tyr Thr Gly Leu Ile Asn Tyr Asp Gly Leu Leu		
190	610	615	620
191	Arg Val Ala His Leu Tyr Ile Met Gly Asn Glu Lys Cys Ser Gln His		
192	625	630	635
193	His Arg Gly Lys Val Thr Leu Asn Glu Ser Glu Ile Cys Ala Gly Ala		640
194	645	650	655
195	Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly Asp Tyr Gly Gly Pro Leu		
196	660	665	670
197	Val Cys Glu Gln His Lys Met Arg Met Val Leu Gly Val Ile Val Pro5		
198	675	680	685
199	Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro Gly Ile Phe Val Arg Val		
200	690	695	700
201	Ala Tyr Tyr Ala Lys Trp Ile His Lys Ile Ile Leu Thr Tyr Lys Val		
202	705	710	715
E-->	203 Pro Gln Ser	723	delete - number the amino acids under every 5 amino acids
250	<210> SEQ ID NO: 4		
251	<211> LENGTH: 39		
252	<212> TYPE: DNA		
253	<213> ORGANISM: Artificial Sequence		insert <2207
W-->	254 <220> FEATURE:		wherever <2217, <2227 or <2237 sequence is shown 39
OK	255 <400> SEQUENCE: 4		(see item 11)
	tgcgctgaca atactatgca agacactgtat gttcccttg		on Error summary sheet)
256	<210> SEQ ID NO: 5		
258	<211> LENGTH: 41		
259	<212> TYPE: DNA		
261	<213> ORGANISM: Artificial Sequence		
W-->	262 <220> FEATURE:	insert <2207	
	<223> OTHER INFORMATION:		
OK	263 <400> SEQUENCE: 5	explain (see item 11)	41
	ggcaaaaatt atatggcca gttatcccaa acaagatctg g		
264	<210> SEQ ID NO: 6		
266	<211> LENGTH: 38		
268	<212> TYPE: DNA		
269	<213> ORGANISM: Artificial Sequence		
W-->	270 <220> FEATURE:	insert <2207	
	<223> OTHER INFORMATION:	see item 11	
OK	271 <400> SEQUENCE: 6		38
	tgcAACACAGG TTCTCCAAGT TTCCCAAGCTG GTATATGG		
272	<210> SEQ ID NO: 7		
274	<211> LENGTH: 38		
276	<212> TYPE: DNA		
277	<213> ORGANISM: Artificial Sequence		
W-->	278 <220> FEATURE:	insert <2207	
	<223> OTHER INFORMATION:	(see item 11)	
OK	279 <400> SEQUENCE: 7		38
	ggGAAGGTGA CTCTGCAAGA GTCTGAAATA TGTGCTGG		
280	<210> SEQ ID NO: 8		

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/582,973

DATE: 06/26/2006  
TIME: 13:30:45

Input Set : A:\sequence list.txt  
Output Set: N:\CRF4\06262006\J582973.raw

283 <211> LENGTH: 38  
284 <212> TYPE: DNA  
285 <213> ORGANISM: Artificial Sequence  
W--> 286 <220> FEATURE: *insert / 2207*  
286 <223> OTHER INFORMATION: *see item 11*  
OK-> 287 <400> SEQUENCE: 8  
288 ggtgatacc a cacc tggaa t agtcaattta gaccatcc

38

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5

<210> 1  
<211> 728  
<212> PRT  
<213> Homo sapiens  
<220> Hepatocyte growth factor  
<223>  
<400> 1

Sapiens

sapience

Hepatocyte growth factor

move to <223> line

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<210> 3  
<211> 2172 *Sapiens*  
<212> DNA  
<213> Homo *sapience*  
<220> Hepatocyte growth factor of five amino acids-deleted type  
<223>  
<400> 3

Move to C2237 line

VERIFICATION SUMMARY DATE: 06/26/2006  
PATENT APPLICATION: US/10/582,973 TIME: 13:30:46

Input Set : A:\sequence list.txt  
Output Set: N:\CRF4\06262006\J582973.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier  
L:4 M:283 W: Missing Blank Line separator, <130> field identifier  
L:5 M:270 C: Current Application Number differs, Replaced Current Application No  
L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:5 M:283 W: Missing Blank Line separator, <160> field identifier  
L:6 M:283 W: Missing Blank Line separator, <210> field identifier  
L:10 M:283 W: Missing Blank Line separator, <220> field identifier  
L:10 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:12 M:283 W: Missing Blank Line separator, <400> field identifier  
L:12 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:11  
L:110 M:283 W: Missing Blank Line separator, <220> field identifier  
L:110 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:112 M:283 W: Missing Blank Line separator, <400> field identifier  
L:112 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:111  
L:203 M:252 E: No. of Seq. differs, <211> LENGTH:Input:723 Found:688 SEQ:2  
L:209 M:283 W: Missing Blank Line separator, <220> field identifier  
L:209 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:211 M:283 W: Missing Blank Line separator, <400> field identifier  
L:211 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:210  
L:254 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4  
L:255 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:4  
L:255 M:283 W: Missing Blank Line separator, <400> field identifier  
L:255 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:254  
L:262 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5  
L:263 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:5  
L:263 M:283 W: Missing Blank Line separator, <400> field identifier  
L:263 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:262  
L:270 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6  
L:271 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:6  
L:271 M:283 W: Missing Blank Line separator, <400> field identifier  
L:271 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:270  
L:278 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:279 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:7  
L:279 M:283 W: Missing Blank Line separator, <400> field identifier  
L:279 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:278  
L:286 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8  
L:287 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:8  
L:287 M:283 W: Missing Blank Line separator, <400> field identifier  
L:287 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:286